TITLE OF THE INVENTION

Method for producing DNA

BACKGROUND OF THE INVENTION

The present invention relates to a method for producing DNA.

As methods for producing DNA, methods based on PCR, methods based on chemical synthesis reactions utilizing automatic synthesizers and so forth are known.

However, when production of DNA having an arbitrary nucleotide sequences is intended, a limitation that DNA having a desired nucleotide sequence should exist beforehand for use as a template, is imposed on the methods based on PCR. Further, in the methods based on chemical synthesis reactions, maximum length of practically producible DNA is limited and therefore production of DNA having a further longer length requires ligation reactions utilizing restriction enzymes and ligases, resulting in a limitation concerning the presence of restriction enzyme recognition sequences.

SUMMARY OF THE INVENTION

An object of the present invention is to provide a method for producing DNA having an arbitrary sequence, which is free from such

limitations as mentioned above.

The inventor of the present invention found that DNA having an arbitrary nucleotide sequence can be synthesized without suffering from such limitations as described above by carrying out steps of preparing oligomers having partial sequences selected according to a specific scheme based on a target nucleotide sequence, and performing PCR using two of single strand DNAs base-paired at their 3' ends as primers and templates to prepare DNA, in a specific manner. Thus, the present invention has been accomplished.

The present invention provides a method for producing DNA, which comprises the following steps (1) to (4) (also referred to as the "first production method of the present invention" hereinafter):

(1) dividing a target sequence which is a nucleotide sequence of DNA to be synthesized into 2N wherein N is a positive integer, of sections, designing partial sequences each containing a nucleotide sequence of each section and a part of a nucleotide sequence of an adjacent section or parts of nucleotide sequences of adjacent sections, wherein the part or parts have such a length that the nucleotide sequence of the each part can specifically make base-pairing with a nucleotide sequence complementary thereto, and

preparing oligomers each having each of the 1st to Nth partial sequences from the 5′ end of the target sequence and oligomers each having a nucleotide sequence complementary to each of the (N+1)th to (2N)th partial sequences from the 5′ end of the target sequence,

(2) performing PCR by using an oligomer having the Nth partial sequence from the 5′ end of the target sequence and an oligomer having a nucleotide sequence complementary to the (N+1)th partial sequence from the 5′ end of the target sequence under such a condition that these oligomers should act as primers and templates,

(3) sequencing synthesized DNAs and selecting DNA having a nucleotide sequence containing the Nth and (N+1)th partial sequences from the 5′ end of the target sequence, and

(4) repeating the following steps (4a) and (4b) for J wherein J is an integer, to be from 1 to N-1:

(4a) performing PCR by using the selected DNA, an oligomer having the (N-J)th partial sequence from the 5′ end of the target sequence and an oligomer having a nucleotide sequence complementary to the (N+1+J)th partial sequence from the 5′ end of the target sequence under such a condition that the DNA and oligomers should act as primers and templates, and

(4b) sequencing synthesized DNAs and selecting DNA having a nucleotide sequence containing the (N-J)th to (N+1+J)th partial sequences.

The present invention further provides a method for producing DNA, which comprises the following steps (1) to (4) (also referred to as the "second production method of the present invention" hereinafter):

(1) dividing a target sequence which is a nucleotide sequence of DNA to be synthesized into 2^n wherein n is a positive integer, of sections, designing partial sequences each containing a nucleotide sequence of each section and a part of a nucleotide sequence of an adjacent section or parts of nucleotide sequences of adjacent sections, wherein the part or parts have such a length that the nucleotide sequence of each part can specifically make base-pairing with a nucleotide sequence complementary thereto, and preparing oligomers each having each of (odd number)th partial sequences from the 5′ end of the target sequence and oligomers each having a nucleotide sequence complementary to each of (even number)th partial sequences from the 5′ end of the target sequence,

(2) repeating the following step (2a) for j wherein j is an integer, to be from 1 to 2^{n-1} to produce 2^{n-1} of reaction products,

(2a) performing PCR by using an oligomer having the (2j-1)th partial sequence from the 5' end of the target sequence and an oligomer having a nucleotide sequence complementary to the (2j)th partial sequence from the 5' end of the target sequence under such a condition that these oligomers should act as primers and templates,
(3) repeating the following step (3a) for i wherein i is an integer, to be from 2 to n:
(3a) repeating the following step (3ai) for k wherein k is an integer, to be from 1 to 2^{n-i} to produce 2^{n-i} of reaction products,
(3ai) mixing a reaction mixture containing DNA having the $(2^i \bullet (k-1)+1)$th to $(2^i \bullet (k-1/2)$th partial sequences from the 5' end of the target sequence and a reaction mixture containing DNA having a sequence complementary to the $(2^i \bullet (k-1/2)+1)$th to $(2^i \bullet k)$th partial sequences from the 5' end of the target sequence and performing PCR under such a condition that DNAs contained in the reaction mixtures should act as primers and templates, and
(4) separating DNAs having a length expected from the target sequence from the reaction mixture, and sequencing the separated double strand DNAs to select a double strand DNA having the target sequence.

In the second production method of the present invention, a ratio of the oligomers added

to the reaction mixture or a ratio of the reaction mixtures to be mixed is preferably adjusted so that a single strand DNA required for a subsequent step should be synthesized in an amount larger than that of the other single strand DNA in the steps (2a) and (3ai).

According to the present invention, there are provided novel methods for producing DNA. According to the first production method of the present invention, there can be practically produced DNA having a length several times larger than the maximum length that can practically be produced by the chemical synthesis method. Further, since restriction enzyme treatment is not essential during the production, the limitation imposed on producible DNA sequence is ameliorated. In addition, in the second production method of the present invention, a cloning step is not included as an intermediate step, and because lengths of the reaction products are approximately doubled in each step, it becomes easy to select the final product. Because of these, rapid and efficient production can be realized.

BRIEF EXPLANATION OF THE DRAWINGS

Fig. 1 shows positional relationship of oligomers in an example of the first production

method of the present invention.

Fig. 2 shows positional relationship of oligomers in an example of the second production method of the present invention and outline of the process.

Fig. 3 shows results of electrophoretic analysis of the PCR products obtained in Example 2 (Tube 1 to Tube 8) (photograph of an electrophoretic image).

DETAILED DESCRIPTION OF THE INVENTION

<First production method of the present invention>

The first production method of the present invention is characterized in that equal numbers of oligomers each having a partial sequence of a target sequence for about half of the 5′ end side of the target sequence and oligomers each having a sequence complementary to a partial sequence of a target sequence for about half of the 3′ end side of the target sequence are prepared so that the partial sequences should have overlaps with adjacent partial sequences, PCR is first performed by using the most internally located two oligomers as primers and templates, and then PCR is repeated by using a reaction product and oligomers located immediately outside the previous ones as primers and templates until the

reaction product should have a length of the target sequence.

Each step of the first production method of the present invention will be explained.

In the step (1), a target sequence which is a nucleotide sequence of DNA to be synthesized is divided into 2N (N is a positive integer) of sections; partial sequences each containing a nucleotide sequence of each section and a part of a nucleotide sequence of an adjacent section or parts of nucleotide sequences of adjacent sections are designed, wherein the part or parts have such a length that the nucleotide sequence of the each part can specifically make base-pairing with a nucleotide sequence complementary thereto; and oligomers each having each of the 1st to Nth partial sequences from the 5′ end of the target sequence and oligomers each having a nucleotide sequence complementary to each of the (N+1)th to (2N)th partial sequences from the 5′ end of the target sequence are prepared. A terminal partial sequence has the part (overlap) only at the internal end, and an internal partial sequence has the parts at the both ends.

The oligomers having a partial sequence or a sequence complementary thereto designed in this step serve as primers and templates in PCR. Therefore, the term "specifically make base-

pairing" means to specifically make base-pairing under the PCR conditions used in the steps (2) and (4a).

A longer partial sequence provides higher efficiency for middle steps. However, the maximum length of DNA practically synthesized by chemical synthesis is limited. Therefore, the length of the partial sequence is usually 150 nucleotides or less, and it is preferably 80-120 nucleotides, if yield, synthesis efficiency and so forth are taken into consideration. In theory, the length of the target sequence is not limited except for a case where the sequence contains repeating sequences. However, if it is taken into consideration that the target sequence is selected by sequence analysis, it is preferably a length that can be determined by once of sequence analysis, and it is usually 1000 nucleotides or less. The number of N is determined based on the lengths of the target sequence and partial sequences as well as overlapping lengths of nucleotide sequences of adjacent sections in the partial sequences.

The overlapping length of nucleotide sequences in partial sequences for adjacent sections may be a length sufficient for the specific base-pairing, and it is usually 17-40 nucleotides. The sequence of the overlap is

selected so that, under the conditions of PCR, formation of primer dimers due to base-pairing at unintended position, intramolecular base-pairing of primer and so forth should be prevented and a suitable denaturation temperature (GC content) should be obtained, as is taken into consideration in the design of primer for usual PCR. All of the lengths of the partial sequences or the overlaps may not be in an equal length, and they may be suitably selected considering the target sequence and the above factors.

In the step (2), PCR is performed by using an oligomer having the Nth partial sequence from the 5' end of the target sequence and an oligomer having a nucleotide sequence complementary to the (N+1)th partial sequence from the 5' end of the target sequence under such a condition that these oligomers should act as primers and templates.

In PCR performed in this step, two kinds of oligomers serve as both of primers and templates, and primers and templates are not distinguished. That is, two kinds of oligomers are base-paired at their 3' ends, and act as both of primers and templates during the extension of each strand.

That is, an oligomer having the Nth partial sequence from the 5' end of the target sequence and an oligomer having a nucleotide sequence complementary to the (N+1)th partial sequence

from the 5' end of the target sequence are added to a reaction mixture where extension reaction by DNA polymerase can be caused, and denaturation reaction, annealing reaction and extension reaction are repeated to synthesize DNA.

The conditions for PCR can be determined by considering factors similar to those of usual PCR.

A typical example of the PCR reaction mixture is a mixture containing 0.5 μM each of oligomers, 20 mM of Tris-HCl (pH 8.3 (25°C)), 1.5 mM of $MgCl_2$, 0.05% of Tween 20, 100 μg/ml of gelatin or BSA, 50 μM each of dNTP and 0.02 units/μl of Taq DNA polymerase (concentrations are final concentrations). The thermal cycle for the reactions may consist of, for example, a cycle of 94-98°C for 30 seconds to 1 minute for denaturation, 50-60°C for 30 seconds to 1 minute for annealing, and 65-72°C for 30 seconds to 1 minute for extension, which is repeated 20 to 30 times, and extension of the final extension reaction for 5 to 10 minutes. Before the cycle, the denaturation reaction may be performed for 2-5 minutes. The reaction is usually stopped by cooling the mixture to 4°C and addition of EDTA (final concentration: 10 mM).

Concentration of dNTP is usually 0.1-0.5 μM. The concentration of dNTP is determined by considering yield of reaction products,

specificity of base-pairing, accuracy of polymerization and so forth.

Magnesium concentration is usually 1.5-3.5 mM. The Mg^{2+} concentration is determined by considering EDTA concentration in the reaction mixture, annealing of primers, denaturation temperature of DNA, specificity of reaction, formation of primer dimer, enzyme activity, accuracy of polymerization and so forth.

Concentration of the primer (oligomer) is usually 0.1-0.5 μM. When the concentration is too high, the specificity of reaction may be reduced, and primer dimer and so forth may be formed.

While concentration of DNA polymerase may vary depending on the type of the polymerase, in case of Taq DNA polymerase, it is usually 1-4 units/100 μl. If the amount of the enzyme is too large, non-specific amplification may occur.

In the first cycle of PCR performed in this step, two kinds of oligomers base-paired at their 3' ends serve as primers and templates, and in the second cycle and thereafter, DNA produced by the extension reaction may be involved in the reaction as a template. That is, there also may occur a reaction in which DNA produced by the extension reaction acts as a template and the oligomers as a whole act as only primer. Therefore, the denaturation conditions are

usually determined so that sufficient denaturation of the DNA that can be a template should be obtained.

The conditions for annealing are determined by considering denaturation temperature, length and concentration of primer and so forth. The temperature is usually, for example, a temperature lower than the denaturation temperature of primer by about 5°C.

The conditions for extension are determined by considering the type of DNA polymerase to be used, length and amount of a portion desired to be extended and temperature. When Taq DNA polymerase is used as the DNA polymerase, the temperature may be its optimal temperature. Since DNA polymerase may be inactivated depending on the denaturation conditions, supplemental addition of DNA polymerase is also taken into consideration.

The above-described PCR can be performed by using widely used apparatuses and enzymes for PCR and so forth as they are.

Further, in such PCR as described above, since DNA used as a template is a single strand DNA, non-specific base-pairing and extension reaction may occur before the temperature reaches the first denaturation temperature, thereby causing non-specific amplification. In such a

case, a technique called hot start method may be used, in which the reaction does not occur until the temperature reaches the first denaturation temperature, and it only occurs after the temperature reaches a predetermined temperature.

In the step (3), the synthesized DNAs are sequenced and DNA having a nucleotide sequence containing the Nth and (N+1)th partial sequences from the 5′ end of the target sequence is selected.

The sequencing of the synthesized DNAs can be performed in a conventional manner. For example, reaction products obtained in the step (2) are subjected to agarose gel electrophoresis, and DNAs having an expected length are extracted from the gel, cloned into a suitable vector, and sequenced. DNA containing the Nth and the (N+1)th partial sequences from the 5′ end of the target sequence may be selected and used in the form of the vector as a template in a subsequent reaction.

In the step (4), the following steps (4a) and (4b) are repeated for J (J is an integer) to be from 1 to N-1.

(4a) PCR is performed by using the selected DNA, an oligomer having the (N-J)th partial sequence from the 5′ end of the target sequence and an oligomer having a nucleotide sequence complementary to the (N+1+J)th partial sequence

from the 5′ end of the target sequence.

(4b) The synthesized DNAs are sequenced and DNA having a nucleotide sequence containing the (N-J)th to (N+1+J)th partial sequences is selected.

In PCR performed in the step (4a), each single strand of DNA and two kinds of oligomers serve as both of primers and templates, and primers and templates are not distinguished. That is, one single strand and one oligomer and the other single strand and the other oligomer are base-paired at their 3′ ends, respectively, and act as both of primers and templates during the extension of each strand.

That is, the selected DNA, an oligomer having the (N-J)th partial sequence from the 5′ end of the target sequence and an oligomer having a nucleotide sequence complementary to the (N+1+J)th partial sequence from the 5′ end of the target sequence are added to a reaction mixture where extension reaction by DNA polymerase can be caused, and denaturation reaction, annealing reaction and extension reaction are repeated to synthesize DNA.

The step (4a) can be performed in the same manner as the step (2) except that a selected DNA is further contained and different oligomers are used. The conditions of PCR are determined by taking these differences into consideration.

However, if the conditions for the step (2) are determined with taking the conditions of the step (4a) into consideration, it can be performed with the same conditions as the step (2).

The step (4b) may be performed in the same manner as the step (3).

Hereafter, the method will be explained with reference to an example where DNA having a nucleotide sequence of 630 nucleotides in length is produced.

The total length is divided into 10 sections (N = 5), and partial sequences are determined with a partial sequence length of 90 nucleotides and an overlap length of 30 nucleotides (Fig. 1). Then, oligomers (U5 to U1) each having each of the first to fifth partial sequences from the 5' end and oligomers (L1 to L5) each having a nucleotide sequence complementary to each of the sixth to tenth partial sequences are synthesized.

By using oligomers U1 and L1, PCR is performed with conditions of 94°C for 2 minutes, subsequent repetition of a cycle of 98°C for 30 seconds, 60°C for 30 seconds and 68°C for 1 minute for 30 times, and 68°C for 10 minutes to synthesize DNA of 150 nucleotides. The obtained DNAs are sequenced, and DNA having an intended sequence is selected.

Then, the following steps (I) to (IV) are

performed.

(I) PCR is performed under the same conditions as mentioned above by using the selected DNA and the oligomers U2 and L2 to synthesize DNA of 270 bp. The obtained DNAs are sequenced, and DNA having an intended sequence is selected.

(II) PCR is performed under the same conditions as mentioned above by using the selected DNA and the oligomers U3 and L3 to synthesize DNA of 390 bp. The obtained DNAs are sequenced, and DNA having an intended sequence is selected.

(III) PCR is performed under the same conditions as mentioned above by using the selected DNA and the oligomers U4 and L4 to synthesize DNA of 510 bp. The obtained DNAs are sequenced, and DNA having an intended sequence is selected.

(IV) PCR is performed under the same conditions as mentioned above by using the selected DNA and the oligomers U5 and L5 to synthesize DNA of 630 bp. The obtained DNAs are sequenced, and DNA having an intended sequence is selected.

In this way, by ligating DNAs obtained through a chemical synthesis method, there can be produced DNA several times longer than the maximum length that can be practically obtained by the chemical synthesis method. And since restriction enzyme treatment is not essential for this method as middle steps, DNA having an

arbitrary sequence can be produced.

<Second production method of the present invention>

The second production method of the present invention is characterized in that equal numbers of oligomers each having a partial sequence of a target sequence and oligomers each having a sequence complementary to a partial sequence of a target sequence are prepared, wherein the former and latter partial sequences are in an alternate positional relationship, so that the partial sequences should have overlaps with adjacent partial sequences; PCR is first performed by using each pair of adjacent oligomers as primers and templates; and then PCR is repeated by using each pair of adjacent reaction products as primers and templates until a reaction product should have a length of the target sequence.

Each step of the second production method of the present invention will be explained.

In the step (1), a target sequence which is a nucleotide sequence of DNA to be synthesized is divided into 2^n (n is a positive integer) of sections; partial sequences each containing a nucleotide sequence of each section and a part of a nucleotide sequence of an adjacent section or parts of nucleotide sequences of adjacent

sections are designed, wherein the part or parts have such a length that the nucleotide sequence of each part can specifically make base-pairing with a nucleotide sequence complementary thereto; and oligomers each having each of (odd number)th partial sequences from the 5′ end of the target sequence and oligomers each having a nucleotide sequence complementary to each of (even number)th partial sequences from the 5′ end of the target sequence are prepared. A terminal partial sequence has the part (overlap) only at the internal end, and an internal partial sequence has the parts at the both ends.

The oligomers having a partial sequence or a sequence complementary thereto determined in this step are used as primers and templates in PCR. Therefore, the term "specifically make base-pairing" means to specifically make base-pairing under the PCR conditions used in the steps (2a) and (3ai).

Length of the partial sequence may be a length of DNA that can practically produced by chemical synthesis, and it is usually 80-120 nucleotides. The number of n is determined based on this length, the length of the target sequence, accuracy of polymerization and so forth, and it is usually 2-4. If it exceeds this range, it may become likely that mutations are introduced, and

thus it may become unlikely that a target sequence can be obtained.

The overlapping length of nucleotide sequences of adjacent sections in the partial sequences may be a length sufficient for the specific base-pairing, and it is usually 17-40 nucleotides. The sequence of the overlap is selected so that, under the conditions of PCR, formation of primer dimers due to base-pairing at unintended position, intramolecular base-pairing of primer and so forth should be prevented and a suitable denaturation temperature (GC content) should be obtained, as is taken into consideration in the design of primer for usual PCR. All of the lengths of the partial sequences or the overlaps may not be in an equal length, and they may be suitably selected considering the target sequence and the above factors. For example, since the length of DNA serving as a primer and a template becomes longer as the reaction steps proceed, the length of the overlap may be changed taking it into consideration.

In the step (2), the following step (2a) is repeated for j (j is an integer) to be from 1 to 2^{n-1} to produce 2^{n-1} of reaction products.
(2a) PCR is performed by using an oligomer having the (2j-1)th partial sequence from the 5′ end of the target sequence and an oligomer having a

nucleotide sequence complementary to the (2j)th partial sequence from the 5' end of the target sequence under such a condition that these oligomers should act as primers and templates.

The step (2a) can be performed in the same manner as the step (2) of the first production method of the present invention. However, the conditions are preferably determined by considering the DNA used in the step (3ai) as primers and templates. Further, EDTA is not added to stop the reaction.

In the step (3), the following step (3a) is repeated for i (i is an integer) to be from 2 to n.

(3a) The following step (3ai) is repeated for k (k is an integer) to be from 1 to 2^{n-i} to produce 2^{n-i} of reaction products.

(3ai) A reaction mixture containing DNA having the $(2^i \cdot (k-1)+1)$th to $(2^i \cdot (k-1/2)$th partial sequences from the 5' end of the target sequence and a reaction mixture containing DNA having a sequence complementary to the $(2^i \cdot (k-1/2)+1)$th to $(2^i \cdot k)$th partial sequences from the 5' end of the target sequence are mixed and PCR is performed under such a condition that DNAs contained in the reaction mixtures should act as primers and templates.

In the step (3ai), reaction mixtures

obtained in a preceding step are mixed to perform PCR. While the reaction conditions for denaturation, annealing, and extension may be the same as those of the step (2a), conditions for a part or all of denaturation, annealing, and extension may be changed depending on the extended length of DNA that serves as primers and templates. Further, depending on the conditions of PCR, other reagents such as DNA polymerase may be added upon mixing of the reaction mixtures.

In the step (4), DNAs having a length expected from the target sequence are separated, and the separated double-strand DNAs are sequenced to select a double-strand DNA having the target sequence.

The separation and sequencing of DNA in the step (4) may be performed in the same manner as the step (3) of the first production method of the present invention.

Hereafter, the method will be explained with reference to an example where DNA having a nucleotide sequence of 500 nucleotides in length is produced.

As shown in the frame in Fig. 2, eight (n = 3) of oligomers (length: 90 nucleotides), Aa1, Aa2, Ab1, Ab2, Ba1, Ba2, Bb1 and Bb2, are prepared. They are designed so that Aa1 and Aa2, Ab1 and Ab2, Ba1 and Ba2, Bb1 and Bb2, Aa2 and

Ab1, and Ba2 and Bb1 should overlap for 30 nucleotides, respectively, and Ab2 and Ba1 should overlap for 40 nucleotides.

First, reaction mixtures containing Aa1 and Aa2, Ab1 and Ab2, Ba1 and Ba2, and Bb1 and Bb2, respectively, are prepared, and PCR is performed for each mixture. After the reaction, the reaction mixture of Aa and the reaction mixture of Ab, and the reaction mixture of Ba and the reaction mixture of Bb are mixed respectively, and PCR is performed for each mixture. After the second reaction, the reaction mixtures obtained after the second reaction are mixed, and PCR is performed. The obtained reaction products are subjected to agarose gel electrophoresis, and DNAs having an expected length are extracted from the gel, cloned into a suitable vector, and sequenced to select a clone of the target sequence.

In the second production method of the present invention, a further longer DNA can be synthesized by increasing the number of steps of the mixing of reaction products. However, it becomes likely that mutations are introduced, and thus it becomes unlikely that DNA having a target sequence can be obtained. By sequencing DNA of about 500 nucleotides once when it is synthesized, and by using it according to other methods, a

further longer final product can be produced.

By the second production method of the present invention, DNA having an arbitrary sequence can also be produced, because restriction enzyme treatment is not essential for this method as middle steps like the first production method of the present invention.

Uncompleted oligomers such as those having a shorter 5'-end-side sequence due to stop of the reaction in their synthesis cycle are not likely to be involved in a reaction in a subsequent step, because they have only a short or no portion for annealing, and thus it is unlikely that clones having deletion should be synthesized. Therefore, the oligomers can be used even with a low purification degree.

Since the length of the reaction product is approximately doubled in every step, the final reaction product shows significant difference in length with respect to other products (e.g., those undergone only reactions of previous steps), and hence it can be easily collected from the gel.

In the second production method of the present invention, a ratio of the oligomers added to the reaction mixture or a ratio of reaction mixtures are preferably adjusted so that a single strand DNA required for a subsequent step should be synthesized in an amount larger than that of

the other single strand DNA in the steps (2a) and (3ai).

A single strand DNA required for a subsequent step is synthesized in an amount larger than that of the other single strand DNA by changing the ratio of the initial amounts of oligomers and the ratios of amounts of the reaction mixtures mixed except for the last mixing of the reaction mixtures, as in the asymmetric PCR (e.g., 1:2-1:9).

A case where the ratio is 1:4 will be explained with reference to Fig. 2. PCR is performed by adding Aa1 and Aa2 in an amount ratio of 4:1, Ab1 and Ab2 in a ratio of 1:4, Ba1 and Ba2 in a ratio of 4:1, and Bb1 and Bb2 in a ratio of 1:4 to a reaction mixture (Ba1 and Ba2, and Bb1 and Bb2 are not shown in the figure). Then, PCR is performed by mixing the reaction mixture of Aa1 and Aa2 and the reaction mixture of Ab1 and Ab2 in a ratio of 4:1. PCR is also performed by mixing the reaction mixture of Ba1 and Ba2 and the reaction mixture of Bb1 and Bb2 in a ratio of 1:4 (not shown in the figure). Subsequently, PCR is performed by mixing the reaction mixture of Aa1 to Ab2 and the reaction mixture of Ba1 to Bb2 in a ratio of 1:1. The obtained reaction products are subjected to agarose gel electrophoresis, and DNAs having an

expected length are extracted from the gel, cloned into a suitable vector, and sequenced to select a clone of the target sequence.

In the second production method of the present invention, the 3' end portion not required to be extended may be modified so that it should not be extended to improve the synthesis efficiency of the target product. While examples of such modification of 3' end include amination, biotinylation, digoxigenylation and so forth, amination that is a small modification in terms of the molecular size is preferred in order not to affect Tm so much.

In the second production method of the present invention, primers of about 20-mer may be designed for the both ends of the synthesized final product and PCR may be performed by using this final product as a template. In this way, the amount of the final product obtained in a small amount may be increased, and products having deletion at the one or both ends may be excluded.

EXAMPLES

Hereafter, the present invention will be explained with reference to the following examples.

Example 1

In order to synthesize DNA having the nucleotide sequence shown in SEQ ID NO: 1 (target sequence), the target sequence was divided into ten sections, and partial sequences of the target sequence were designed with a length of 90 nucleotides and overlap of adjacent sections of 30 nucleotides. Further, oligomers each having each of the partial sequences of the target sequence (U1 to U5) and oligomers each having a sequence complementary to each of the partial sequences of the target sequence (L1 to L5) were synthesized. The nucleotide sequences of U1 to U5 and L1 to L5 are shown in SEQ ID NOS: 2-11, respectively. The positional relationship of U1 to U5 and L1 to L5 is shown in Fig. 1.

For reaction, 25 μl of a reaction mixture containing 0.4 μM each of U1 and L1, 40 mM of Tricine-KOH (pH 9.2 at 25°C), 15 mM of potassium acetate (KOAc), 1.5 mM of magnesium acetate ($Mg(OAc)_2$), 75 μg/ml of bovine serum albumin (BSA) and 0.2 mM each of dNTP and 0.5 μl of Advantage KlenTaq Polymerase Mix was prepared by using a PCR kit produced by Clontech Co., Advantage cDNA PCR Kit.

The reaction was performed under the following conditions.

The reaction mixture was kept at 94°C for 2

minutes, and then subjected to a cycle of denaturation reaction at 98°C for 30 seconds, annealing reaction at 60°C for 30 seconds and extension reaction at 68°C for 1 minute, which was repeated 30 times, and then final extension reaction was extended for 10 minutes. The reaction was stopped by cooling the reaction mixture to 4°C.

The obtained reaction product was separated by agarose gel electrophoresis, and fragments having a length expected from the nucleotide sequences of U1 and L1 were extracted from the gel and purified. The obtained fragments were directly cloned by using a vector kit for TA cloning, pGEM-T Vector System (Promega).

Inserted sequences were determined for a part of the obtained clones. As a result, clones having the nucleotide sequences shown in Table 1 were obtained. In Table 1, the target sequence is shown in the top line. The parenthesized numbers indicate designations of the clones, and a designation to which "*" is appended on the right side indicates a clone having a target sequence.

The clone having the target sequence was used for the subsequent reaction. The same reaction mixture as mentioned above except that it contained about 5 ng of this plasmid and U2 and L2 instead of U1 and L1 was prepared, and a

reaction product was obtained with the same reaction conditions as those mentioned above.

The obtained reaction product was separated by agarose gel electrophoresis, and fragments having a length expected from the nucleotide sequences of U1, U2, L1 and L2 were extracted from the gel and purified. The obtained fragments were directly cloned by using a vector kit for TA cloning, pGEM-T Vector System (Promega).

Inserted sequences were determined for a part of the obtained clones. As a result, clones having the nucleotide sequences shown in Table 2 were obtained. In Table 2, the target sequence is shown in the top line. The parenthesized numbers indicate designations of the clones, and a designation to which "*" is appended on the right side indicates a clone having a target sequence.

The clone having the target sequence was used for the subsequent reaction. The same reaction mixture as mentioned above was prepared except that it contained about 5 ng of this plasmid and U3 and L3 instead of U1 and L1, and a reaction product was obtained with the same reaction conditions as those mentioned above.

The obtained reaction product was separated by agarose gel electrophoresis, and fragments having a length expected from the nucleotide sequences of U1 to U3 and L1 to L3 were extracted

from the gel and purified. The obtained fragments were directly cloned by using a vector kit for TA cloning, pGEM-T Vector System (Promega).

Inserted sequences were determined for a part of the obtained clones. As a result, clones having the nucleotide sequences shown in Table 3 were obtained. In Table 3, the target sequence is shown in the top line. The parenthesized numbers indicate designations of the clones, and a designation to which "*" is added on the right side indicates a clone having a target sequence.

The clone having the target sequence was used for the subsequent reaction. The same reaction mixture as mentioned above was prepared except that it contained about 5 ng of this plasmid, and U4 and L4 instead of U1 and L1, and a reaction product was obtained with the same reaction conditions as those mentioned above.

The obtained reaction product was separated by agarose gel electrophoresis, and fragments having a length expected from the nucleotide sequences of U1 to U4 and L1 to L4 were extracted from the gel and purified. The obtained fragments were directly cloned by using a vector kit for TA cloning, pGEM-T Vector System (Promega).

Inserted sequences were determined for a part of the obtained clones. As a result, clones having the nucleotide sequences shown in Table 4

were obtained. In Table 4, the target sequence is shown in the top line. The parenthesized numbers indicate designations of the clones, and a designation to which "*" is appended on the right side indicates a clone having a target sequence.

The clone having the target sequence was used for the subsequent reaction. The same reaction mixture as mentioned above was prepared except that it contained about 5 ng of this plasmid, and U5 and L5 instead of U1 and L1, and a reaction product was obtained with the same reaction conditions as those mentioned above.

The obtained reaction product was separated by agarose gel electrophoresis, and fragments having a length expected from the nucleotide sequences of U1 to U5 and L1 to L5 were extracted from the gel and purified. The obtained fragments were directly cloned by using a vector kit for TA cloning, pGEM-T Vector System (Promega).

Inserted sequences were determined for a part of the obtained clones. As a result, clones having the nucleotide sequences shown in Table 5 were obtained. In Table 5, the target sequence is shown in the top line. The parenthesized numbers indicate designations of the clones, and a designation to which "*" is appended on the right side indicates a clone having a target sequence.

In this way, DNA having a target sequence

could be produced.

Table 1

		10	20	30	40	50	
U1L1	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(01)	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(02)	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TAGGCACGTT	GGGACAGAAA	50
U1L1(03)	1	AAGATCCTT-	----------	----------	----------	----------	50
U1L1(04)	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGACA	50
U1L1(06)	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(07)*	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(08)*	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(09)	1	AAGATCCCTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(10)	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(11)	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(12)	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(13)	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(14)*	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(15)	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(18)	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(19)	1	AAGATCCTTC	TTATTCCCAA	CCCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(20)	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(21)	1	AAGATCCTTC	TTATTCCCAA	-CCAGCATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(23)	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(24)*	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(25)	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(26)	1	AAGATCCTTC	TTATTCC-AA	-CCAGGAT--	-GGGCACGTT	GGGACAGAAA	50
U1L1(27)	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	-GGGCACGTT	GGGACAGAAA	50
U1L1(28)	1	AAGATCCTTC	TTATTCCCAA	ACCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(29)	1	AAGATCCTT-	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(30)*	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(31)	1	AAGATCCTTC	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(32)	1	----------	----------	----------	----------	-------AAA	50
U1L1(33)	1	AAGATCCTTC	TTATTCCCAA	-CCAGGA---	----------	----------	50
U1L1(34)	1	AAGA-CCT-C	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50
U1L1(35)	1	AAGATCCTTC	TTATTCC-AA	-CCAG-----	----------	----------	50
U1L1(36)	1	AAGATCCTT-	TTATTCCCAA	-CCAGGATGA	TGGGCACGTT	GGGACAGAAA	50

Table 1 (continued)

```
                  60         70         80         90        100
U1L1      51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(01)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GAT------- ---------- 100
U1L1(02)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(03)  51 ---------- ------TCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(04)  51 TGCTTGACTT ATGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(06)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(07)* 51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(08)* 51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(09)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(10)  51 TGCTTGACTT CTGGGGTC-- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(11)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(12)  51 TGCTT----- CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(13)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTAT--- 100
U1L1(14)* 51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(15)  51 TGCTTGACTT CTGGGGTCCC ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(18)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(19)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(20)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(21)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(23)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(24)* 51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(25)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(26)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(27)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(28)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(29)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(30)* 51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(31)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(32)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(33)  51 -GCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(34)  51 TGCTTGACTT CTGGGGTC-- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(35)  51 ------ACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
U1L1(36)  51 TGCTTGACTT CTGGGGTCC- ACTTTTCTGG GATGTTTTCT AAACTATCAG 100
```

Table 1 (continued)

		110	120	130	140	150	
U1L1	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(01)	101	----------	--------AC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(02)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(03)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(04)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(06)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAG--	150
U1L1(07)*	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(08)*	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(09)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(10)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(11)	101	GGC-------	----------	----------	----------	----------	150
U1L1(12)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(13)	101	----------	-----AACAC	-ATCAGTATA	ACATC-----	--------GA	150
U1L1(14)*	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(15)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(18)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	----------	--------GA	150
U1L1(19)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(20)	101	GGCTGTCGAT	GGTAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(21)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(23)	101	GGCTGTCGAG	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(24)*	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(25)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGT-T	CTGGGTAGGA	150
U1L1(26)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGATAGGA	150
U1L1(27)	101	GGCTGTCGAT	GGAAAAACAC	-AGCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(28)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(29)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(30)*	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(31)	101	GGCTGTCGAT	GGAAAAACAC	CATCAGTATA	ACATCGGTAT	GTGGGTAGGA	150
U1L1(32)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(33)	101	GGCTGTCGAT	GGAAAAA---	----------	----------	-------GGA	150
U1L1(34)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(35)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150
U1L1(36)	101	GGCTGTCGAT	GGAAAAACAC	-ATCAGTATA	ACATCGGTAT	CTGGGTAGGA	150

Table 1 (continued)

```
                    160        170        180        190        200
U1L1       151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(01)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(02)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(03)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(04)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(06)   151 ---..... ..... ..... ..... ..... ..... ..... 200
U1L1(07)*  151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(08)*  151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(09)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(10)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(11)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(12)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(13)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(14)*  151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(15)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(18)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(19)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(20)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(21)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(23)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(24)*  151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(25)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(26)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(27)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(28)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(29)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(30)*  151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(31)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(32)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(33)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(34)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(35)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
U1L1(36)   151 GAG..... ..... ..... ..... ..... ..... ..... 200
```

Table 2

```
                 10         20         30         40         50
U2L2        1 AGGTTTCACC GGCTCCTGCT TCATCTTGGC TAGCTCCCGC CTTGT-GTGC  50
U2L2(02)    1 ---------- ---------- ---------- ---------- ----------  50
U2L2(05)    1 ---------- ---------- ---------- ---------- ----------  50
U2L2(10)    1 ---------- ---------- ---------- ---------- ----------  50
U2L2(12)    1 ---------- ---------- ---------- ---------- ----------  50
U2L2(13)    1 ---------- ---------- ---------- ---------- ----------  50
U2L2(15)    1 ---------- ---------- ---------- ---------- ----------  50
U2L2(16)    1 ---------- ---------- ---------- ---------- ----------  50
U2L2(17)    1 ---------- ---------- ---------- ---------- ----------  50
U2L2(18)    1 ---------- ---------- ---------- ---------- ----------  50
U2L2(01)    1 AGGTTTCACC GGCTCCTGCT TCATCTTGGC TAGCTCCCGC CTTGT-GTGC  50
U2L2(03)    1 AGGTTTCACC GGCTCCTGCT TCATCTTGGC TAGCTCCCGC CTTGT-G-GC  50
U2L2(04)    1 AGGTTTCACC GGCTCCTGCT TCATCTTGGC TAGCTCCCGC CTTGT-GTGC  50
U2L2(06)    1 AGGTTTCACC GGCTCCTGCT TCATCTTGGC TAGCTCCCGC CTTGT-GTGC  50
U2L2(07)    1 ---------- ---------- ---------- ---------- ----------  50
U2L2(08)    1 AGGTTTCACC GGCTCCTGCT TCATCTTGGC TAGCTCCCGC CTTGT-GTGC  50
U2L2(09)*   1 AGGTTTCACC GGCTCCTGCT TCATCTTGGC TAGCTCCCGC CTTGT-GTGC  50
U2L2(11)    1 AGGTTTCACC GGCTCCTGCT TCATCTTGGC TAGCTCCCGC CTTGT-GTGC  50
U2L2(14)    1 AGGTTTCACC GGCTCCTGCT TCATCTTGGC TAGCTCCCGC CTTGTGTGTC  50
U2L2(19)    1 AGGTTTCACC GGCTCCTTCT T--------- ---------- ----------  50
U2L2(20)    1 ---------- ---------- ---------- ----------  -------TGC  50
U2L2(22)    1 AGGTTTCACC GGCTCCTGCT TCATCTTGGC TAGCTCCCGC CTTGT-GTGC  50
U2L2(23)    1 AGGTTTCACC G-CTCCTGCT TCATCTTGGC TAGCTCCCGC CTTGT-GTGC  50
U2L2(24)    1 AGGTTTCACC GGCTCCTGCT TCATCTTGGC TAGCTCCCGC CTTGT-GTGC  50
```

Table 2 (continued)

```
                 60         70         80         90        100
U2L2       51 TCATCATTCC GAAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(02)   51 ---------- -AAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(05)   51 ---------- -AAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(10)   51 ---------- -AAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(12)   51 ---------- -AAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(13)   51 ---------- -AAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(15)   51 ---------- -AAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(16)   51 ---------- -AAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(17)   51 ---------- -AAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(18)   51 ---------- -AAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(01)   51 TCATCATTCC GAAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(03)   51 TCATCATTCC GAAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(04)   51 TCATCATTCC GAAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(06)   51 TCATCATTCC GAAGATCCTT CTTATTCCCA AC-AGGATGA TGGGCACGTT 100
U2L2(07)   51 ---------- ----ATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(08)   51 TCATCATTCC GCAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(09)*  51 TCATCATTCC GAAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(11)   51 TCATCATTCC GAAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(14)   51 TCATCATTCC GAAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(19)   51 ---------- ---------- ---ATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(20)   51 TCATCATTCC GAAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(22)   51 TCATCATTCT GAAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(23)   51 TCATCATTCC GAAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
U2L2(24)   51 TCATCATTCC GAAGATCCTT CTTATTCCCA ACCAGGATGA TGGGCACGTT 100
```

Table 2 (continued)

		110	120	130	140	150	
U2L2	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(02)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(05)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(10)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(12)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(13)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(15)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(16)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(17)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(18)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(01)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(03)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(04)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(06)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(07)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(08)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(09)*	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(11)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(14)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(19)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(20)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(22)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(23)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150
U2L2(24)	101	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	CTTTTCTGGG	ATGTTTTCTA	150

Table 2 (continued)

		160	170	180	190	200	
U2L2	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(02)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(05)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(10)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(12)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(13)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(15)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(16)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(17)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(18)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(01)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(03)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(04)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(06)	151	AACTATCAGG	GCGGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(07)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(08)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(09)*	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(11)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCG	200
U2L2(14)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(19)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(20)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(22)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(23)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200
U2L2(24)	151	AACTATCAGG	GCTGTCGATG	GAAAAACACA	TCAGTATAAC	ATCGGTATCT	200

Table 2 (continued)

		210	220	230	240	250	
U2L2	201	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	TCTTCCTGCC	CAGCTGTGTC	250
U2L2(02)	201	GGGTAGGAGA	G---------	----------	----------	----------	250
U2L2(05)	201	GGGTAGGAGA	G---------	----------	----------	----------	250
U2L2(10)	201	GGGTAGGAGA	G---------	----------	----------	----------	250
U2L2(12)	201	GGGTAGGAGA	G---------	----------	----------	----------	250
U2L2(13)	201	GGGTAGGAGA	G---------	----------	----------	----------	250
U2L2(15)	201	GGGTAGGAGA	G---------	----------	----------	----------	250
U2L2(16)	201	GGGTAGGAGA	G---------	----------	----------	----------	250
U2L2(17)	201	GGGTAGGAGA	G---------	----------	----------	----------	250
U2L2(18)	201	GGGTAGGAGA	G---------	----------	----------	----------	250
U2L2(01)	201	GGGTAGGAGA	GGGGCC....	....	....	....	250
U2L2(03)	201	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	TCTTCCTGCC	CAGCTGTGTC	250
U2L2(04)	201	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	TCTTCCTGCC	CAGCTGGGTC	250
U2L2(06)	201	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	TCTTCCTGCC	CAGCTGTGTC	250
U2L2(07)	201	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	TCTTCCTGCC	CAGCTGTGTC	250
U2L2(08)	201	GGGTAGGAGA	GGGGCCTCAG	GCGATCACAA	TCTTCCTGCC	CAGCTGTGTC	250
U2L2(09)*	201	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	TCTTCCTGCC	CAGCTGTGTC	250
U2L2(11)	201	GGGTAGGAGA	GGGACCTCAG	GCGATCATAA	ACTT------	----------	250
U2L2(14)	201	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	TCTTCCTGCC	CAGCTGTGTC	250
U2L2(19)	201	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	TCTTCCTGCC	CAGCTGTGTC	250
U2L2(20)	201	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	TCTTCCTGCC	CAGCTGTGTC	250
U2L2(22)	201	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	TCTTCCTGCC	CAGCTGTGTC	250
U2L2(23)	201	GGGTAGGAGA	GGGGCCTCAA	GCGATCATAA	TCTTCCTGCC	CAGCTGTGTC	250
U2L2(24)	201	GGGTAGGAGA	GGGGCCGCAC	G-GATCATAA	TCTTCCTGCC	CAGCTGTGTC	250

Table 2 (continued)

		260	270	280	290	300	
U2L2	251	CCACAAAGCC	AACTCTACCT	G.........	....	....	300
U2L2(02)	251	----------	----------	-.........	....	....	300
U2L2(05)	251	----------	----------	-.........	....	....	300
U2L2(10)	251	----------	----------	-.........	....	....	300
U2L2(12)	251	----------	----------	-.........	....	....	300
U2L2(13)	251	----------	----------	-.........	....	....	300
U2L2(15)	251	----------	----------	-.........	....	....	300
U2L2(16)	251	----------	----------	-.........	....	....	300
U2L2(17)	251	----------	----------	-.........	....	....	300
U2L2(18)	251	----------	----------	-.........	....	....	300
U2L2(01)	251	....	....	....	....	....	300
U2L2(03)	251	CCACAAAGCC	AACTCTACCT	G.........	....	....	300
U2L2(04)	251	CCACAAAGCC	AACTCTACCT	G.........	....	....	300
U2L2(06)	251	CCACAAAGCC	AACTCTACCT	G.........	....	....	300
U2L2(07)	251	CCACAAAGCC	AACTCTACCT	G.........	....	....	300
U2L2(08)	251	CCACAAAGCC	AACTCTACCT	G.........	....	....	300
U2L2(09)*	251	CCACAAAGCC	AACTCTACCT	G.........	....	....	300
U2L2(11)	251	----------	-ACTCTACCT	G.........	....	....	300
U2L2(14)	251	CCACAAAGCC	AACTCTACCT	G.........	....	....	300
U2L2(19)	251	CCACAAAGCC	AACTCTACCT	G.........	....	....	300
U2L2(20)	251	CCACAAAGCC	AACTCTACCT	G.........	....	....	300
U2L2(22)	251	CCACAAAGCC	AACTCTACCT	G.........	....	....	300
U2L2(23)	251	CCACAAAGCC	AACTCTACCT	G.........	....	....	300
U2L2(24)	251	CCACAAAGCC	AACTCTACCT	G.........	....	....	300

Table 3

		10	20	30	40	50	
U3L3	1	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	AATCCTGTTT	GCCATATCTC	50
U3L3(02)	1	----------	----------	----------	----------	----------	50
U3L3(04)	1	----------	----------	----------	----------	----------	50
U3L3(23)	1	----------	----------	----------	----------	----------	50
U3L3(29)	1	----------	----------	----------	----------	----------	50
U3L3(01)	1	----------	----------	-AAAAGCGCC	AATCCTGTTT	GCCATATCTC	50
U3L3(03)	1	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	AATCCTGTTT	GCCATA----	50
U3L3(05)	1	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	AATCCTGTTT	GCCATATCTC	50
U3L3(06)*	1	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	AATCCTGTTT	GCCATATCTC	50
U3L3(07)	1	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	AATCCTGTTT	GCCATATCTC	50
U3L3(09)	1	----------	----------	----------	-------TTT	GCCATATCTC	50
U3L3(10)*	1	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	AATCCTGTTT	GCCATATCTC	50
U3L3(11)	1	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	AATCCTGTTT	GCCATATCTC	50
U3L3(12)*	1	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	AATCCTGTTT	GCCATATCTC	50
U3L3(13)	1	TGCTGAAC-C	TCCATGTACC	CAAAAGCGCC	AATCCTGTTT	GCCATATCTC	50
U3L3(14)	1	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	AATCCTGTTT	GCCATATCTC	50
U3L3(15)	1	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	AATCCTGTTT	GCCATATCTC	50
U3L3(16)	1	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	AATCCTGTTT	GCCATATCTC	50
U3L3(17)	1	TGCTGAACAC	TC-ATGTACC	CAAAAGCGCC	AATCCTGTTT	GCCATATCTC	50
U3L3(18)	1	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	AATCCTGTTT	ACCATATCTC	50
U3L3(19)	1	----------	----------	----------	----------	----------	50
U3L3(20)	1	----------	----------	------CGCC	AATCCTGTTT	GCCATATCTC	50
U3L3(21)	1	----------	----------	----AGCGCC	AATCCTGTTT	GCCATATCTC	50
U3L3(22)	1	----------	----------	----------	----------	----------	50
U3L3(24)	1	---------C	TCC-TG-ACC	CAAAAGCGCC	AATCCTGTTT	GCCATATCTC	50
U3L3(25)	1	----------	----------	----------	----------	----------	50
U3L3(26)	1	--CTGAACAC	TCCATGTACC	CAAAAGCGCC	AATCCTGTTT	GCCATATCTC	50
U3L3(28)	1	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	AATCCTGTTT	GCCATATCTC	50

Table 3 (continued)

		60	70	80	90	100	
U3L3	51	TGCCTTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(02)	51	----------	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(04)	51	----------	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(23)	51	----------	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(29)	51	----------	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(01)	51	TGCCTTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(03)	51	---CTTCTTC	AGGTTTCACT	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(05)	51	TGCCTTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCGTGGC	TAGCTCCCGC	100
U3L3(06)*	51	TGCCTTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(07)	51	TGCCTTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(09)	51	TGCCTTCT-C	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(10)*	51	TGCCTTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(11)	51	TGCCTTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(12)*	51	TGCCTTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(13)	51	TGCCTTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(14)	51	TGCTGTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(15)	51	TGCCTTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(16)	51	TGCCTTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(17)	51	TGCCTTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(18)	51	TGCCTTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(19)	51	----------	--GTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(20)	51	TGCCTTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TTGCTCCCGC	100
U3L3(21)	51	TGCCTTCTTC	AGGTTT-ACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(22)	51	----------	-GGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(24)	51	TGCCTTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(25)	51	----------	-GGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(26)	51	TGCCTTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100
U3L3(28)	51	TGCCTTCTTC	AGGTTTCACC	GGCTCCTGCT	TCATCTTGGC	TAGCTCCCGC	100

Table 3 (continued)

		110	120	130	140	150	
U3L3	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(02)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(04)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(23)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(29)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(01)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(03)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(05)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(06)*	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(07)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(09)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(10)*	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(11)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(12)*	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(13)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(14)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(15)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(16)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(17)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(18)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(19)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(20)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(21)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(22)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(24)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(25)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(26)	101	CTTGTGTGCT	CATCATTCCG	AAGATCCTTC	TTATTCCCAA	CCAGGATGAT	150
U3L3(28)	101	CTTGTGTGCT	CATCATTCCG	AGGATCCTTC	TTATTCCCAA	CCAGGATGAT	150

Table 3 (continued)

		160	170	180	190	200	
U3L3	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(02)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(04)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(23)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(29)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(01)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(03)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(05)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(06)*	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(07)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(09)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(10)*	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(11)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(12)*	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(13)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(14)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(15)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(16)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(17)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(18)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(19)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(20)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(21)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(22)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(24)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(25)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(26)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200
U3L3(28)	151	GGGCACGTTG	GGACAGAAAT	GCTTGACTTC	TGGGGTCCAC	TTTTCTGGGA	200

Table 3 (continued)

		210	220	230	240	250	
U3L3	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(02)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(04)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(23)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(29)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(01)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(03)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(05)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(06)*	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(07)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(09)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(10)*	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(11)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(12)*	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(13)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(14)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(15)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(16)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(17)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(18)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(19)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(20)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(21)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGAATAACA	250
U3L3(22)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(24)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(25)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(26)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250
U3L3(28)	201	TGTTTTCTAA	ACTATCAGGG	CTGTCGATGG	AAAAACACAT	CAGTATAACA	250

Table 3 (continued)

		260	270	280	290	300	
U3L3	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(02)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(04)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(23)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(29)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(01)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(03)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(05)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(06)*	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(07)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(09)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(10)*	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(11)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(12)*	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(13)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(14)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(15)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(16)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(17)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(18)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(19)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(20)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(21)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(22)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(24)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(25)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(26)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300
U3L3(28)	251	TCGGTATCTG	GGTAGGAGAG	GGGCCTCAGG	CGATCATAAT	CTTCCTGCCC	300

Table 3 (continued)

		310	320	330	340	350	
U3L3	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(02)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	----------	----------	350
U3L3(04)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	----------	----------	350
U3L3(23)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	----------	----------	350
U3L3(29)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	----------	----------	350
U3L3(01)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(03)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(05)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(06)*	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(07)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(09)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(10)*	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(11)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACTTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(12)*	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(13)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(14)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(15)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(16)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(17)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(18)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(19)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(20)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(21)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTGCATCC	ACCTCGATAT	350
U3L3(22)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(24)	301	AGCTGTGGCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(25)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(26)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350
U3L3(28)	301	AGCTGTGTCC	CACAAAGCCA	ACTCTACCTG	CTTTCCATCC	ACCTCGATAT	350

Table 3 (continued)

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                    360        370        380        390        400
U3L3        351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(02)    351 ---------- ---------- ---------- ---------- --..... 400
U3L3(04)    351 ---------- ---------- ---------- ---------- --..... 400
U3L3(23)    351 ---------- ---------- ---------- ---------- --..... 400
U3L3(29)    351 ---------- ---------- ---------- ---------- --..... 400
U3L3(01)    351 CTGCCACATA G---TCAAAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(03)    351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(05)    351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACCC TC..... 400
U3L3(06)*   351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(07)    351 CTGCCACATA GTTCTCAAAC CACTGTGGGC ACATACACC- TC..... 400
U3L3(09)    351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(10)*   351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(11)    351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(12)*   351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(13)    351 CTGCCACATA GTTCTCAAAC -ACTGGGGGC ACATACACC- TC..... 400
U3L3(14)    351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(15)    351 CTGC------ ---------- ---TGTGGGC ACATACACC- TC..... 400
U3L3(16)    351 CTGCCACATA GTTCTCAATC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(17)    351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(18)    351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(19)    351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(20)    351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(21)    351 C--------- -------GAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(22)    351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(24)    351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(25)    351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(26)    351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACC- TC..... 400
U3L3(28)    351 CTGCCACATA GTTCTCAAAC -ACTGTGGGC ACATACACC- TC..... 400
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Table 4

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                10         20         30         40         50
U4L4         1 AGCTTGCAGA G-CAGCTCTC GTAGCCATTT CAAAAACCTC TCTCACTCCA  50
U4L4(01)     1 ---------- ---------- ---------- -----ACCTC TCTCACTCCA  50
U4L4(02)     1 ---------- G-CAGCTCTC GTAGCCATTT CAAAAACCTC TCTCACTCCA  50
U4L4(03)*    1 AGCTTGCAGA G-CAGCTCTC GTAGCCATTT CAAAAACCTC TCTCACTCCA  50
U4L4(04)*    1 AGCTTGCAGA G-CAGCTCTC GTAGCCATTT CAAAAACCTC TCTCACTCCA  50
U4L4(05)     1 AGCTTGCAGA GGCAGCTCTC GTAGCCATTT CAAAAACCTC TCTCACTCCA  50
U4L4(08)     1 ---------- ---------- ---------- ---------- ----------  50
U4L4(10)     1 ------CAGA G-CAGCTCTC GTAGCCATTT CAAAAACCTC TCTCACTCCA  50
U4L4(11)     1 AGCTTGCAGA G-CAGCTCTC GTAGCCATTT CAAAAACCTC TCTCACTCCA  50
U4L4(13)     1 AGCTTGCAGA G-CAGCTCTC GTAGCCATTT CAAAAACCTC TCTCACTCCA  50
U4L4(15)*    1 AGCTTGCAGA G-CAGCTCTC GTAGCCATTT CAAAAACCTC TCTCACTCCA  50
U4L4(16)*    1 AGCTTGCAGA G-CAGCTCTC GTAGCCATTT CAAAAACCTC TCTCACTCCA  50
U4L4(17)     1 ---------- ---------- ---------- ---------- ----------  50
U4L4(18)*    1 AGCTTGCAGA G-CAGCTCTC GTAGCCATTT CAAAAACCTC TCTCACTCCA  50
U4L4(19)     1 AGCTTGCAGA G-CAGCTCTC GTAGCCATTT CAAAAACCTC TCTCACTCCA  50
U4L4(20)     1 AGCTTGCAGA G-CAGCTCTC GTAGCCATTT CAAAAACCTC TCTCACTCCA  50
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Table 4 (continued)

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                60         70         80         90        100
U4L4        51 TCTTTGGTCT TTGCTGAACA CTCCATGTAC CCAAAAGCGC CAATCCTGTT 100
U4L4(01)    51 TCTTTGGTCT TTGCTGAACA CTCCATGTAC CCAAAAGCGC CAATCCTGTT 100
U4L4(02)    51 TCTTTGGTCT TTGCTGAACA CTCCATGTAC CCAAAAGCGC CAATCCTGTT 100
U4L4(03)*   51 TCTTTGGTCT TTGCTGAACA CTCCATGTAC CCAAAAGCGC CAATCCTGTT 100
U4L4(04)*   51 TCTTTGGTCT TTGCTGAACA CTCCATGTAC CCAAAAGCGC CAATCCTGTT 100
U4L4(05)    51 TCTTTGGTCT TTGCTGAACA CTCCATGTAC CCAAAAGCGC CAATCCTGTT 100
U4L4(08)    51 ---------- ---------- ---------C CCAAAAGCGC CAATCCTGTT 100
U4L4(10)    51 TCTTTGGTCT TTGCTGAACA CTCCATGTAC CCAAAAGCGC CAATCCTGTT 100
U4L4(11)    51 TCTTTGGTCT TTGCTGAACA CTCCATGTAC CCAAA-GCGC CAATCCTGTT 100
U4L4(13)    51 TCTTTGGTCT TTGCTGAACA CTCCATGTAC CCAAA-GCGC CAATCCTGTT 100
U4L4(15)*   51 TCTTTGGTCT TTGCTGAACA CTCCATGTAC CCAAAAGCGC CAATCCTGTT 100
U4L4(16)*   51 TCTTTGGTCT TTGCTGAACA CTCCATGTAC CCAAAAGCGC CAATCCTGTT 100
U4L4(17)    51 ---------- ---------- ---------C CCAAAAGCGC CAATCCTGTT 100
U4L4(18)*   51 TCTTTGGTCT TTGCTGAACA CTCCATGTAC CCAAAAGCGC CAATCCTGTT 100
U4L4(19)    51 TCTTTGGTCT TTGCTGAACA CTCCATGTAC CCAAAAGCGC CAATCCTGTT 100
U4L4(20)    51 TCTTTGGTCT TTGCTGAACA CTCCATGTAC CCAAAAGCGC CAATCCTGTT 100
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Table 4 (continued)

		110	120	130	140	150	
U4L4	101	TGCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	TTCATCTTGG	150
U4L4(01)	101	TGCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	TTCATCTTGG	150
U4L4(02)	101	TGCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	TTCATCTTGG	150
U4L4(03)*	101	TGCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	TTCATCTTGG	150
U4L4(04)*	101	TGCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	TTCATCTTGG	150
U4L4(05)	101	TGCCATATCT	CTGCCTTCTT	CAG-TTTCAC	CGGCTCCTGC	TTCATCTTGG	150
U4L4(08)	101	TGCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	TTCATCTTGG	150
U4L4(10)	101	TGCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	TTCATCTTGG	150
U4L4(11)	101	TGCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	TTCATCTTGG	150
U4L4(13)	101	TGCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	TTCATCTTGG	150
U4L4(15)*	101	TGCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	TTCATCTTGG	150
U4L4(16)*	101	TGCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	TTCATCTTGG	150
U4L4(17)	101	TGCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	TTCATCTTGG	150
U4L4(18)*	101	TGCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	TTCATCTTGG	150
U4L4(19)	101	TGCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	TTCATCTTGG	150
U4L4(20)	101	TGCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	TTCATCTTGG	150

Table 4 (continued)

		160	170	180	190	200	
U4L4	151	CTAGCTCCCG	CCTTGTGTGC	TCATCATTCC	GAAGATCCTT	CTTATTCCCA	200
U4L4(01)	151	CTAGCTCCCG	CCTTGTGTGC	TCATCATTCC	GAAGATCCTT	CTTATTCCCA	200
U4L4(02)	151	CTAGCTCCCG	CCTTGTGTGC	TCATCATTCC	GAAGATCCTT	CTTATTCCCA	200
U4L4(03)*	151	CTAGCTCCCG	CCTTGTGTGC	TCATCATTCC	GAAGATCCTT	CTTATTCCCA	200
U4L4(04)*	151	CTAGCTCCCG	CCTTGTGTGC	TCATCATTCC	GAAGATCCTT	CTTATTCCCA	200
U4L4(05)	151	CTAGCTCCCG	CCTTGTGTGC	TCATCATTCC	GAAGATCCTT	CTTATTCCCA	200
U4L4(08)	151	CTAGCTCCCG	CCTTGTGTGC	TCATCATTCC	GAAGATCCTT	CTTATTCCCA	200
U4L4(10)	151	CTAGCTCCCG	CCTTGTGTGC	TCATCATTCC	GAAGATCCTT	CTTATTCCCA	200
U4L4(11)	151	CTAGCTCCCG	CCTTGTGTGC	TCATCATTCC	GAAGATCCTT	CTTATTCCCA	200
U4L4(13)	151	CTAGCTCCCG	CCTTGTGTGC	TCATCATTCC	GAAGATCCTT	CTTATTCCCA	200
U4L4(15)*	151	CTAGCTCCCG	CCTTGTGTGC	TCATCATTCC	GAAGATCCTT	CTTATTCCCA	200
U4L4(16)*	151	CTAGCTCCCG	CCTTGTGTGC	TCATCATTCC	GAAGATCCTT	CTTATTCCCA	200
U4L4(17)	151	CTAGCTCCCG	CCTTGTGTGC	TCATCATTCC	GAAGATCCTT	CTTATTCCCA	200
U4L4(18)*	151	CTAGCTCCCG	CCTTGTGTGC	TCATCATTCC	GAAGATCCTT	CTTATTCCCA	200
U4L4(19)	151	CTAGCTCCCG	CCTTGTGTGC	TCATCATTCC	GAAGATCCTT	CTTATTCCCA	200
U4L4(20)	151	CTAGCTCCCG	CCTTGTGTGC	TCATCATTCC	GAAGATCCTT	CTTATTCCCA	200

Table 4 (continued)

		210	220	230	240	250	
U4L4	201	ACCAGGATGA	TGGGCACGTT	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	250
U4L4(01)	201	ACCAGGATGA	TGGGCACGTT	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	250
U4L4(02)	201	ACCAGGATGA	TGGGCACGTT	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	250
U4L4(03)*	201	ACCAGGATGA	TGGGCACGTT	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	250
U4L4(04)*	201	ACCAGGATGA	TGGGCACGTT	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	250
U4L4(05)	201	ACCAGGATGA	TGGGCACGTT	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	250
U4L4(08)	201	ACCAGGATGA	TGGGCACGTT	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	250
U4L4(10)	201	ACCAGGATGA	TGGGCACGTT	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	250
U4L4(11)	201	ACCAGGATGA	TGGGCACGTT	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	250
U4L4(13)	201	ACCAGGATGA	TGGGCACGTT	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	250
U4L4(15)*	201	ACCAGGATGA	TGGGCACGTT	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	250
U4L4(16)*	201	ACCAGGATGA	TGGGCACGTT	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	250
U4L4(17)	201	ACCAGGATGA	TGGGCACGTT	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	250
U4L4(18)*	201	ACCAGGATGA	TGGGCACGTT	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	250
U4L4(19)	201	ACCAGGATGA	TGGGCACGTT	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	250
U4L4(20)	201	ACCAGGATGA	TGGGCACGTT	GGGACAGAAA	TGCTTGACTT	CTGGGGTCCA	250

Table 4 (continued)

		260	270	280	290	300	
U4L4	251	CTTTTCTGGG	ATGTTTTCTA	AACTATCAGG	GCTGTCGATG	GAAAAACACA	300
U4L4(01)	251	CTTTTCTGGG	ATGTTTTCTA	AACTATCAGG	GCTGTCGATG	GAAAAACACA	300
U4L4(02)	251	CTTTTCTGGG	ATGTTTTCTA	AACTATCAGG	GCTGTCGATG	GAAAAACACA	300
U4L4(03)*	251	CTTTTCTGGG	ATGTTTTCTA	AACTATCAGG	GCTGTCGATG	GAAAAACACA	300
U4L4(04)*	251	CTTTTCTGGG	ATGTTTTCTA	AACTATCAGG	GCTGTCGATG	GAAAAACACA	300
U4L4(05)	251	CTTTTCTGGG	ATGTTTTCTA	AACTATCAGG	GCTGTCGATG	GAAAAACACA	300
U4L4(08)	251	CTTTTCTGGG	ATGTTTTCTA	AACTATCAGA	GCTGTCGATG	GAAAAACACA	300
U4L4(10)	251	CTTTTCTGGG	ATGTTTTCTA	AACTATCAGG	GCTGTCGATG	GAAAAACACA	300
U4L4(11)	251	CTTTTCTGGG	ATGTTTTCTA	AACTATCAGG	GCTGTCGATG	GAAAAACACA	300
U4L4(13)	251	CTTTTCTGGG	ATGTTTTCTA	AACTATCAGG	GCTGTCGATG	GAAAAACACA	300
U4L4(15)*	251	CTTTTCTGGG	ATGTTTTCTA	AACTATCAGG	GCTGTCGATG	GAAAAACACA	300
U4L4(16)*	251	CTTTTCTGGG	ATGTTTTCTA	AACTATCAGG	GCTGTCGATG	GAAAAACACA	300
U4L4(17)	251	CTTTTCTGGG	ATGTTTTCTA	AACTATCAGA	GCTGTCGATG	GAAAAACACA	300
U4L4(18)*	251	CTTTTCTGGG	ATGTTTTCTA	AACTATCAGG	GCTGTCGATG	GAAAAACACA	300
U4L4(19)	251	CTTTTCTGGG	ATGTTTTCTA	AACTATCAGG	GCTGTCGATG	GAAAAACACA	300
U4L4(20)	251	CTTTTCTGGG	ATGTTTTCTA	AACTATCAGG	GCTGTCGATG	GAAAAACACA	300

Table 4 (continued)

		310	320	330	340	350	
U4L4	301	TCAGTATAAC	ATCGGTATCT	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	350
U4L4(01)	301	TCAGTATAAC	ATCGGTATCT	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	350
U4L4(02)	301	TCAGTATAAC	ATCGGTATCT	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	350
U4L4(03)*	301	TCAGTATAAC	ATCGGTATCT	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	350
U4L4(04)*	301	TCAGTATAAC	ATCGGTATCT	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	350
U4L4(05)	301	TCAGTATAAC	ATCGGTATCT	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	350
U4L4(08)	301	TCAGTATAAC	ATCGGTATCT	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	350
U4L4(10)	301	TCAGTATAAC	ATCGGTATCT	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	350
U4L4(11)	301	TCAGTATAAC	ATCGGTATCT	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	350
U4L4(13)	301	TCAGTATAAC	ATCGGTATCT	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	350
U4L4(15)*	301	TCAGTATAAC	ATCGGTATCT	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	350
U4L4(16)*	301	TCAGTATAAC	ATCGGTATCT	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	350
U4L4(17)	301	TCAGTATAAC	ATCGGTATCT	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	350
U4L4(18)*	301	TCAGTATAAC	ATCGGTATCT	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	350
U4L4(19)	301	TCAGTGTAAC	ATCGGTATCT	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	350
U4L4(20)	301	TCAGTGTAAC	ATCGGTATCT	GGGTAGGAGA	GGGGCCTCAG	GCGATCATAA	350

Table 4 (continued)

		360	370	380	390	400	
U4L4	351	TCTTCCTGCC	CAGCTGTGTC	CCACAAAGCC	AACTCTACCT	GCTTTCCATC	400
U4L4(01)	351	TCTTCCTGCC	CAGCTGTGTC	CCACAAAGCC	AACTCTACCT	GCTTTCCATC	400
U4L4(02)	351	TCTTCCTGCC	CAGCTGTGTC	CCACAAAGCC	AACTCTACCT	GCTTTCCATC	400
U4L4(03)*	351	TCTTCCTGCC	CAGCTGTGTC	CCACAAAGCC	AACTCTACCT	GCTTTCCATC	400
U4L4(04)*	351	TCTTCCTGCC	CAGCTGTGTC	CCACAAAGCC	AACTCTACCT	GCTTTCCATC	400
U4L4(05)	351	TCTTCCTGCC	CAGCTGTGTC	CCACAAAGCC	AACTCTACCT	GCTTTCCATC	400
U4L4(08)	351	TCTTCCTGCC	CAGCTGTGTC	CCACAAAGCC	AACTCTACCT	GCTTTCCATC	400
U4L4(10)	351	TCTTCCTGCC	CAGCTGTGTC	CCACAAAGCC	AACTCTACCT	GCTTTCCATC	400
U4L4(11)	351	TCTTCCTGCC	CAGCTGTGTC	CCACAAAGCC	AACTCTACCT	GCTTTCCATC	400
U4L4(13)	351	TCTTCCTGCC	CAGCTGTGTC	CCACAAAGCC	AACTCTACCT	GCTTTCCATC	400
U4L4(15)*	351	TCTTCCTGCC	CAGCTGTGTC	CCACAAAGCC	AACTCTACCT	GCTTTCCATC	400
U4L4(16)*	351	TCTTCCTGCC	CAGCTGTGTC	CCACAAAGCC	AACTCTACCT	GCTTTCCATC	400
U4L4(17)	351	TCTTCCTGCC	CAGCTGTGTC	CCACAAAGCC	AACTCTACCT	GCTTTCCATC	400
U4L4(18)*	351	TCTTCCTGCC	CAGCTGTGTC	CCACAAAGCC	AACTCTACCT	GCTTTCCATC	400
U4L4(19)	351	TCTTCCTGCC	CAGCTGTGTC	CCACAAAGCC	AACTCTACCT	GCTTTCCATC	400
U4L4(20)	351	TCTTCCTGCC	CAGCTGTGTC	CCACAAAGCC	AACTCTACCT	GCTTTCCATC	400

Table 4 (continued)

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                  410        420        430        440        450
U4L4      401 CACCTCGATA TCTGCCACAT AGTTCTCAAA CACTGTGGGC ACATACACCT 450
U4L4(01)  401 CACCTCGATA TCTGCCACAT AGTTCTCAAA CACTGTGGGC ACATACACCT 450
U4L4(02)  401 CACCTCGATA TCTGCCACAT AGTTCTCAAA CACTGTGGGC ACATACACCT 450
U4L4(03)* 401 CACCTCGATA TCTGCCACAT AGTTCTCAAA CACTGTGGGC ACATACACCT 450
U4L4(04)* 401 CACCTCGATA TCTGCCACAT AGTTCTCAAA CACTGTGGGC ACATACACCT 450
U4L4(05)  401 CACCTCGATA TCTGCCACAT AGTTCTCAAA CACTGTGGGC ACATACACCT 450
U4L4(08)  401 CACCTCGATA TCTGCCACAT AGTTCTCAAA CACTGTGGGC ACATACACCT 450
U4L4(10)  401 CACCTCGATA TCTGCCACAT AGTTCTCAAA CACTGTGGGC ACATACACCT 450
U4L4(11)  401 CACCTCGATA TCTGCCACAT AGTTCTCAAA CACTGTGGGC ACATACACCT 450
U4L4(13)  401 CACCTCGATA TCTGCCACAT AGTTCTCAAA CACTGTGGGC ACATACACCT 450
U4L4(15)* 401 CACCTCGATA TCTGCCACAT AGTTCTCAAA CACTGTGGGC ACATACACCT 450
U4L4(16)* 401 CACCTCGATA TCTGCCACAT AGTTCTCAAA CACTGTGGGC ACATACACCT 450
U4L4(17)  401 CACCTCGATA TCTGCCACAT AGTTCTCAAA CACTGTGGGC ACATACACCT 450
U4L4(18)* 401 CACCTCGATA TCTGCCACAT AGTTCTCAAA CACTGTGGGC ACATACACCT 450
U4L4(19)  401 CACCTCGATA TCTGCCACAT AGTTCTCAAA CACTGTGGGC ACATACACCT 450
U4L4(20)  401 CACCTCGATA TCTGCCACAT AGTTCTCAAA CACTGTGGGC ACATACACCT 450
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Table 4 (continued)

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                  460        470        480        490        500
U4L4      451 CTGGGAACTG GTCCTTGCTG AAGACTATTA ATAGGCATGT CTTTCCACAG 500
U4L4(01)  451 CTGGGAACTG GTCCTTGCTG AAGACTATTA ATAGGCATGT CTTTCCACAG 500
U4L4(02)  451 CTGGGAACTG GTCCTTGCTG AAGACTATTA ATAGGCATGT CTTTCCACAG 500
U4L4(03)* 451 CTGGGAACTG GTCCTTGCTG AAGACTATTA ATAGGCATGT CTTTCCACAG 500
U4L4(04)* 451 CTGGGAACTG GTCCTTGCTG AAGACTATTA ATAGGCATGT CTTTCCACAG 500
U4L4(05)  451 CTGGGAACTG GTCCTTGCTG AAGACTATTA ATAGGCATGT CTTTCCACAG 500
U4L4(08)  451 GTGGGAACTG GTCCTTGCTG AAGACTATTA ATAGGCATGT CTTTCCACAG 500
U4L4(10)  451 CTGGGAACTG GGCCTTGCTG AAGACTATTA ATAGGCATGT CTTTCCACAG 500
U4L4(11)  451 CTGGGAACTG GTCCTTGCTG AAGACTATTA ATAGGCATGT CTTTCCACAG 500
U4L4(13)  451 CTGGGAACTG GTCCTTGCTG AAGACTATTA ATAGGCATGT CTTTCCACAG 500
U4L4(15)* 451 CTGGGAACTG GTCCTTGCTG AAGACTATTA ATAGGCATGT CTTTCCACAG 500
U4L4(16)* 451 CTGGGAACTG GTCCTTGCTG AAGACTATTA ATAGGCATGT CTTTCCACAG 500
U4L4(17)  451 GTGGGAACTG GTCCTTGCTG AAGACTATTA ATAGGCATGT CTTTCCACAG 500
U4L4(18)* 451 CTGGGAACTG GTCCTTGCTG AAGACTATTA ATAGGCATGT CTTTCCACAG 500
U4L4(19)  451 CTGGGAACTG GTCCTTGCTG AAGACTATTA ATAGGCATGT CTTTCCACAG 500
U4L4(20)  451 CTGGGAACTG GTCCTTGCTG AAGACTATTA ATAGGCATGT CTTTCCACAG 500
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Table 4 (continued)

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                    510         520         530         540         550
U4L4       501 GCTACATCAC C......... .......... .......... .......... 550
U4L4(01)   501 GCTACATCAC C......... .......... .......... .......... 550
U4L4(02)   501 GCTACATCAC C......... .......... .......... .......... 550
U4L4(03)*  501 GCTACATCAC C......... .......... .......... .......... 550
U4L4(04)*  501 GCTACATCAC C......... .......... .......... .......... 550
U4L4(05)   501 GCTACATCAC C......... .......... .......... .......... 550
U4L4(08)   501 GCTACATCAC C......... .......... .......... .......... 550
U4L4(10)   501 GCTACATCAC C......... .......... .......... .......... 550
U4L4(11)   501 GCTACATCAC C......... .......... .......... .......... 550
U4L4(13)   501 GCTACATCAC C......... .......... .......... .......... 550
U4L4(15)*  501 GCTACATCAC C......... .......... .......... .......... 550
U4L4(16)*  501 GCTACATCAC C......... .......... .......... .......... 550
U4L4(17)   501 GCTACATCAC C......... .......... .......... .......... 550
U4L4(18)*  501 GCTACATCAC C......... .......... .......... .......... 550
U4L4(19)   501 GCTACATCAC C......... .......... .......... .......... 550
U4L4(20)   501 GCTACATCAC C......... .......... .......... .......... 550
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Table 5

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                10         20         30         40         50
U5L5         1 GGCTCGAGGT ACCGCGGCCG CTCACAAGAC AAGGCAACCA GATTTTTTCT  50
U5L5(01)     1 ---------- ---------- ---------- ---------- ----------  50
U5L5(02)     1 ---------- ---------- ---------- ---------- ----------  50
U5L5(03)     1 ---------- ---------- ---------- ---------- ----------  50
U5L5(05)     1 ---------- ---------- -----AAGAC AAGGCAACCA GATTTTTTCT  50
U5L5(06)     1 ---------- ---------- ---------- -AGGCAACCA GATTTTTTCT  50
U5L5(07)     1 ---------- ---------- ---------- ---------- ----------  50
U5L5(08)     1 GGCTCGAGGT ACCGCGGCCG CTCACAAGAC AAGGCAACCA GATTTTTTCT  50
U5L5(09)     1 ---------- ---------- ---------- ---------- ----------  50
U5L5(10)     1 GGCTCGAGGT ACCGCGGCCG CTCACAAGAC AAGGCAACCA GATTTTTTCT  50
U5L5(11)     1 GGCTCGAGGT ACCGCGGCCG CT-------- ---------- ----------  50
U5L5(12)     1 ---------- ---------- --------AC AAGGCAACCA GATTTTTTCT  50
U5L5(13)*    1 GGCTCGAGGT ACCGCGGCCG CTCACAAGAC AAGGCAACCA GATTTTTTCT  50
U5L5(15)     1 GGCTCGAGGT ACCGCGGCCG CTCACAAGAC AAGGCAACCA GATTTTTTCT  50
U5L5(16)     1 ---------- ---------- ---------- ----CAACCA AATTTTTTCT  50
U5L5(17)     1 ----CGAGGT ACCGCGGCCG CTCACAAGAC AAGGCAACCA AATTTTTTCT  50
U5L5(18)     1 GGCTCGAGGT ACCGCGGCCG CTCACAAGAC AAGGCAACCA GATTTTTTCT  50
U5L5(19)     1 -------GGT ACCGCGGCCG CTCACAAGAC AAGGCAACCA GATTTTTTCT  50
U5L5(21)     1 ---------T ACCGCGGCCG CTCACAAGAC AAGGCAACCA GATTTTTTCT  50
U5L5(23)     1 ---------- ---------- ---------- ---------- ----------  50
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Table 5 (continued)

		60	70	80	90	100	
U5L5	51	TCCCACGTCT	AGCTTGCAGA	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(01)	51	----------	----------	-CAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(02)	51	-----CGTCT	AGCTTGCAGA	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(03)	51	----------	---------A	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(05)	51	TCCCACGTCT	AGCTTGCAGA	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(06)	51	TCCCACGTCT	AGCTTGCAGA	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(07)	51	----------	----------	---GCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(08)	51	TCCCACGTCT	AGCTTGCAGA	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(09)	51	----------	----------	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(10)	51	TCCCACGTCT	AGCTTGCAGA	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(11)	51	----------	--------GA	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(12)	51	TCCCACGTCT	AGCTTGCAGA	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(13)*	51	TCCCACGTCT	AGCTTGCAGA	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(15)	51	TCCCACGTCT	AGCTTGCAGA	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(16)	51	TCCCACGTCT	AGCTTGCAGA	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(17)	51	TCCCACGTCT	AGCTTGCAGA	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(18)	51	TCCCACGTCT	AGCTTGCAGA	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(19)	51	TCCCACGTCT	AGCTTGCAGA	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(21)	51	TCCCACGTCT	AGCTTGCAGA	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100
U5L5(23)	51	----------	---------A	GCAGCTCTCG	TAGCCATTTC	AAAAACCTCT	100

Table 5 (continued)

		110	120	130	140	150	
U5L5.	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(01)	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(02)	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(03)	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(05)	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(06)	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(07)	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(08)	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(09)	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(10)	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(11)	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(12)	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(13)*	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(15)	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(16)	101	CCCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(17)	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(18)	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(19)	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(21)	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150
U5L5(23)	101	CTCACTCCAT	CTTTGGTCTT	TGCTGAACAC	TCCATGTACC	CAAAAGCGCC	150

Table 5 (continued)

		160	170	180	190	200	
U5L5	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(01)	151	AATCCTGTTT	TGCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(02)	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(03)	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(05)	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(06)	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(07)	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(08)	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(09)	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(10)	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(11)	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(12)	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(13)*	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(15)	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(16)	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTTAC	CGGCTCCTGC	200
U5L5(17)	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(18)	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(19)	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(21)	151	AATCCTGTTT	-GCCATATCT	CTGCCTTTTT	CAGGTTTCAC	CGGCTCCTGC	200
U5L5(23)	151	AATCCTGTTT	-GCCATATCT	CTGCCTTCTT	CAGGTTTCAC	CGGCTCCTGC	200

Table 5 (continued)

		210	220	230	240	250	
U5L5	201	TTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(01)	201	TTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(02)	201	TTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(03)	201	TTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(05)	201	TTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(06)	201	TTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(07)	201	TTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(08)	201	TTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(09)	201	TTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(10)	201	TTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(11)	201	TTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(12)	201	TTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(13)*	201	TTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(15)	201	TTCATCTCGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(16)	201	TTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(17)	201	TTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(18)	201	CTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(19)	201	TTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(21)	201	TTCATCTTGG	-CTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250
U5L5(23)	201	TTCATCTTGG	ACTAGCTCCC	GCCTTGTGTG	CTCATCATTC	CGAAGATCCT	250

Table 5 (continued)

		260	270	280	290	300	
U5L5	251	TCTTATTCCC	AACCCGGATG	ATGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(01)	251	TCTTATTCCC	AACCCGGATG	ATGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(02)	251	TCTTATTCCC	AACCCGGATG	ATGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(03)	251	TCTTATTCCC	AACCCGGATG	GTGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(05)	251	TCTTATTCCC	AACCCGGATG	ATGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(06)	251	TCTTATTCCC	AACCCGGATG	ATGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(07)	251	TCTTATTCCC	AACCCGGATG	ATGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(08)	251	TCTTATTCCC	AACCCGGATG	ATGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(09)	251	TCTTATTCCC	AACCCGGATG	ATGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(10)	251	TCTTATTCCC	AACCCGGATG	ATGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(11)	251	TCTTATTCCC	AACCCGGATG	ATGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(12)	251	TCTTATTCCC	AACCCGGATG	ATGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(13)*	251	TCTTATTCCC	AACCCGGATG	ATGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(15)	251	TCTTATTCCC	AACCCGGATG	ATAGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(16)	251	TCTTATTCCC	AACCCGGATG	ATGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(17)	251	TCTTATTCCC	AACCCGGATG	ATGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(18)	251	TCTTATTCCC	AACCCGGATG	ATGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(19)	251	TCTTATTCCC	AACCCGGATG	ATGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(21)	251	TCTTATTCCC	AACCCGGATG	ATGGGCACGT	TGGGACAGAA	ATGCTTGACT	300
U5L5(23)	251	TCTTATTCCC	AACCCGGATG	GTGGGCACGT	TGGGACAGAA	ATGCTTGACT	300

Table 5 (continued)

		310	320	330	340	350	
U5L5.	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(01)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(02)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(03)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(05)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(06)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(07)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(08)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(09)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(10)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(11)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(12)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(13)*	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(15)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(16)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(17)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(18)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(19)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350
U5L5(21)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCGG	GGCTGTCGAT	350
U5L5(23)	301	TCTGGGGTCC	ACTTTTCTGG	GATGTTTTCT	AAACTATCAG	GGCTGTCGAT	350

Table 5 (continued)

		360	370	380	390	400	
U5L5	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(01)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(02)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(03)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(05)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(06)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(07)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(08)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(09)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(10)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(11)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(12)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(13)*	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(15)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(16)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(17)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(18)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(19)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(21)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400
U5L5(23)	351	GGAAAAACAC	ATCAGTATAA	CATCGGTATC	TGGGTAGGAG	AGGGGCCTCA	400

Table 5 (continued)

		410	420	430	440	450	
U5L5.	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(01)	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(02)	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(03)	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(05)	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(06)	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(07)	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(08)	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(09)	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(10)	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(11)	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(12)	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(13)*	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(15)	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(16)	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(17)	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(18)	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(19)	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(21)	401	GGCGATCATA	ATCTTCC-TG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450
U5L5(23)	401	GGCGATCATA	ATCTTCCATG	CCCAGCTGTG	TCCCACAAAG	CCAACTCTAC	450

Table 5 (continued)

		460	470	480	490	500	
U5L5	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(01)	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(02)	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(03)	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTTTCA	AACACTGTGG	500
U5L5(05)	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(06)	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(07)	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(08)	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(09)	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(10)	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(11)	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(12)	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(13)*	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(15)	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(16)	451	CTGCTTTCCA	TCCACCTCGA	TATTTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(17)	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(18)	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(19)	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(21)	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTCTCA	AACACTGTGG	500
U5L5(23)	451	CTGCTTTCCA	TCCACCTCGA	TATCTGCCAC	ATAGTTTTCA	AACACTGTGG	500

Table 5 (continued)

		510	520	530	540	550	
U5L5	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550
U5L5(01)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550
U5L5(02)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAGTAGGCAT	550
U5L5(03)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550
U5L5(05)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550
U5L5(06)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550
U5L5(07)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550
U5L5(08)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550
U5L5(09)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550
U5L5(10)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550
U5L5(11)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550
U5L5(12)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TANTAGGCAT	550
U5L5(13)*	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550
U5L5(15)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550
U5L5(16)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550
U5L5(17)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550
U5L5(18)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550
U5L5(19)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550
U5L5(21)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550
U5L5(23)	501	GCACATACAC	CTCTGGGAAC	TGGTCCTTGC	TGAAGACTAT	TAATAGGCAT	550

Table 5 (continued)

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                  560        570        580        590        600
U5L5       551 GTCTTTCCAC AGGCTACATC ACCAACAATC ACCAGTTTCT TCCGGTTCAG 600
U5L5(01)   551 GTCTTTCCAC AGGCTACATC ACCAACAATC ACCAGTTTCT TCCGGTTCAG 600
U5L5(02)   551 GTCTTTCCAC AGGCTACATC ACCAACAATC ACCAGTTTCT TCCGGTTCAG 600
U5L5(03)   551 GTCTTTCCAC AGGCTACATC ACCAACAATC ACCAGTTTCT TCCGGTTCAG 600
U5L5(05)   551 GTCTTTCCAC AGGCTACATC ACCAACAATC ACCAGTTTCT TCCGGTTCAG 600
U5L5(06)   551 GTCTTTCCAC AGGCTACATC ACCAACAATC ACCAGTTTCT TCCGGTTCAG 600
U5L5(07)   551 GTCTT-CCAC AGGCTACATC ACCAACAATC ACCAGTT--- ---------- 600
U5L5(08)   551 GTCTTTCCAC AGGCTACATC ACCAACAATC ACCAGTTTCT TCCGGTTCAG 600
U5L5(09)   551 GTCTTTCCAC AGGCTACATC ACCAACAATC ACCAGTTTCT TCCGGTTCAG 600
U5L5(10)   551 GTCTTTCCAC AGGCTACATC ACCAACAATT ACCAGTTTCT TCCGGTTCAG 600
U5L5(11)   551 GTCTTTCCAC AGGCTACATC A--------- ---------- ---------- 600
U5L5(12)   551 GTCTTTCCAC AGGCTACATC ACCAACAATC ACCAGTTTCT TCCGGTTCAG 600
U5L5(13)*  551 GTCTTTCCAC AGGCTACATC ACCAACAATC ACCAGTTTCT TCCGGTTCAG 600
U5L5(15)   551 GTCTTTCCAC AGGC------ ---------- ---------- ---------- 600
U5L5(16)   551 GTCTTTCCAC AGGCTACATC ACCAACAATC ACCAGTT--- ---------- 600
U5L5(17)   551 GTCTTTCCAC AGGCTACATC ACCAACAATC ACCAGTTTCT TCCGG----- 600
U5L5(18)   551 GTCTTTCCAC AGGCTACA-- ---------- ---------- ---------- 600
U5L5(19)   551 GTCTTTCCAC AGGCTACATC ACCAACAATC ACCAGTTTCT TC-------- 600
U5L5(21)   551 GTCTTTCCAC AGGCTACATC ACCAACAATC ACCAGTTTCT TCCGGTTCAG 600
U5L5(23)   551 GTCTTTCCAC AGGCTACATC ACCAACAATC ACCAGTTTCT TCCGGTTCAG 600
```

Table 5 (continued)

```
                  610        620        630        640        650
U5L5       601 GTCCTCCTCG GAGATCAGCT TCTGCT-CCA TGGG..... ..... 650
U5L5(01)   601 GTCCTCCTTG GAGATCAGCT TCTGCT-CCA TGGG..... ..... 650
U5L5(02)   601 GTC------- ---------- ---------- ----..... ..... 650
U5L5(03)   601 GTCCTCCTCG GAGATCAGCT TCTGCTTCCA TGGG..... ..... 650
U5L5(05)   601 GTCCT----- ---------- ---------- ----..... ..... 650
U5L5(06)   601 GTCCTCCT-- ---------- ---------- ----..... ..... 650
U5L5(07)   601 ---------- ---------- ---------- ----..... ..... 650
U5L5(08)   601 GT-------- ---------- ---------- ----..... ..... 650
U5L5(09)   601 GTCCTCCTCG GAGATCAGCT TCTGCT-CCA TGGG..... ..... 650
U5L5(10)   601 GTCCTCCTCG GAGATCAGCT TC..... ..... ..... ..... 650
U5L5(11)   601 ---------- ---------- ---------- ---..... ..... 650
U5L5(12)   601 GTCCTCCTCG GAGATCAGCT TCTGCT-CCA TGGG..... ..... 650
U5L5(13)*  601 GTCCTCCTCG GAGATCAGCT TCTGCT-CCA TGGG..... ..... 650
U5L5(15)   601 ---------- ---------- ---------- ----..... ..... 650
U5L5(16)   601 ---------- ---------- ---------- ----..... ..... 650
U5L5(17)   601 ---------- ---------- ---------- ----..... ..... 650
U5L5(18)   601 ---------- ---------- ---------- ----..... ..... 650
U5L5(19)   601 ---------- ---------- ---------- ----..... ..... 650
U5L5(21)   601 GTCCTCCTCG GAGATCAGCT TCTGCT-CCA TGGG..... ..... 650
U5L5(23)   601 GTCCTCCTCG GAGATCAGCT TCTGCTTCCA TGGG..... ..... 650
```

Example 2

In order to synthesize DNA having the nucleotide sequence shown in SEQ ID NO: 12 (target sequence), oligomers having a length of 104 nucleotides, 1a, 1b, 2a, 2b, 3a, 3b, 4a and 4b were synthesized, each of which had each of the nucleotide sequences shown in SEQ ID NOS: 13-20. These oligomers correspond to Aa1, Aa2, Ab1, Ab2, Ba1, Ba2, Bb1 and Bb2, respectively, which are shown in the frame in Fig. 2.

Reaction mixtures having each of the compositions shown in Table 6 were prepared in four of tubes (Tube 1 to Tube 4), and PCR was performed by leaving at 94°C for 1 minute, and repeating 30 times a cycle of reactions at 94°C for 1 minute and 68°C for 30 seconds. In this stage, a fragment of 179 bp is synthesized.

Table 6

Composition of reaction mixture (unit: μl)

	Tube 1	Tube 2	Tube 3	Tube 4
10 x Pyrobest PCR reaction buffer	10	10	10	10
2.5 mM dNTP mixture	2	2	2	2
Primer a (10 pmol/μl)	4(1a)	1(2a)	4(3a)	1(4a)
Primer b (10 pmol/μl)	1(1b)	4(2b)	1(3b)	4(4b)
Pyrobest DNA polymerase (5 unit/μl)	0.5	0.5	0.5	0.5
Water	82.5	82.5	82.5	82.5
Total	100	100	100	100

After completion of the reaction, portions of 80 μl and 20 μl were taken out from Tube 1 and Tube 2, respectively, and mixed in a new tube (Tube 5). Similarly, portions of 20 μl and 80 μl were taken out from Tube 3 and Tube 4, respectively, and mixed in a new tube (Tube 6). The mixtures in Tube 5 and Tube 6 were allowed to react under the same conditions as described above. In this stage, a fragment of 326 bp is synthesized.

After completion of the reaction, portions of 50 μl and 50 μl were taken out from Tube 5 and Tube 6, respectively, and mixed in a new tube (Tube 7). The mixture in Tube 7 was allowed to react under the same conditions as described

above. In this stage, a fragment of 612 bp is synthesized.

Then, the target fragment was amplified. Based on the sequences of the both ends of the target sequence, oligomers of 20-mer having the nucleotide sequences shown in SEQ ID NOS: 21 and 22, respectively, were prepared. These oligomers were used as primers (Upper and Lower), and a reaction mixture having the composition shown in Table 7 mentioned below was prepared (Tube 8). PCR was performed by leaving at 98°C for 1 minute, and repeating 30 times a cycle of reactions at 98°C for 30 seconds and 68°C for 90 seconds.

Table 7

Composition of reaction mixture (unit: μl)

10 x Pyrobest PCR reaction buffer	10
Reaction product of Tube 7	4
2.5 mM dNTP mixture	2
Primer Upper (10 pmol/μl)	5
Primer Lower (10 pmol/μl)	5
Pyrobest DNA polymerase (5 unit/μl)	0.5
Water	73.5
Total	100

After the reaction described above, 5 μl each of the reaction products of Tube 1 to Tube 8 were subjected to agarose gel electrophoresis to

confirm the amplification (Fig. 3). Since the amplification was confirmed, a target length of the reaction product obtained in Tube 8 was collected from the electrophoresis gel, and directly cloned by using pGEM-T Vector System (Promega).

Fifteen of the obtained clones were sequenced. As a result, one clone having the target sequence was obtained.

SEQUENCE LISTING

<110> AOTSUKA, Satoshi

<120> Method for producing DNA

<130>

<150> JP 2000-229284
<151> 2000-07-28

<160> 22

<210> 1
<211> 630
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 1
ggctcgaggt accgcggccg ctcacaagac aaggcaacca gatttttct tcccacgtct 60
agcttgcaga gcagctctcg tagccatttc aaaaacctct ctcactccat ctttggtctt 120
tgctgaacac tccatgtacc caaaagcgcc aatcctgttt gccatatctc tgccttcttc 180
aggtttcacc ggctcctgct tcatcttggc tagctcccgc cttgtgtgct catcattccg 240
aagatccttc ttattcccaa cccggatgat gggcacgttg ggacagaaat gcttgacttc 300
tggggtccac ttttctggga tgtttttctaa actatcaggg ctgtcgatgg aaaaacacat 360
cagtataaca tcggtatctg ggtaggagag gggcctcagg cgatcataat cttcctgccc 420
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gttctcaaac actgtgggca catacacctc tgggaactgg tccttgctga agactattaa 540
taggcatgtc tttccacagg ctacatcacc aacaatcacc agtttcttcc ggttcaggtc 600
ctcctcggag atcagcttct gctccatggg 630

<210> 2
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 2
aagatccttc ttattcccaa ccaggatgat gggcacgttg ggacagaaat gcttgacttc 60
tggggtccac ttttctggga tgttttctaa 90

<210> 3
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 3

aggtttcacc ggctcctgct tcatcttggc tagctcccgc cttgtgtgct catcattccg 60
aagatccttc ttattcccaa ccaggatgat 90

<210> 4
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 4
tgctgaacac tccatgtacc caaaagcgcc aatcctgttt gccatatctc tgccttcttc 60
aggtttcacc ggctcctgct tcatcttggc 90

<210> 5
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 5
agcttgcaga gcagctctcg tagccatttc aaaaacctct ctcactccat ctttggtctt 60
tgctgaacac tccatgtacc caaaagcgcc 90

<210> 6
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 6
ggctcgaggt accgcggccg ctcacaagac aaggcaacca gatttttttct tcccacgtct 60
agcttgcaga gcagctctcg tagccatttc 90

<210> 7
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 7
ctctcctacc cagataccga tgttatactg atgtgttttt ccatcgacag ccctgatagt 60
ttagaaaaca tcccagaaaa gtggacccca 90

<210> 8
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 8
caggtagagt tggctttgtg ggacacagct gggcaggaag attatgatcg cctgaggccc 60
ctctcctacc cagataccga tgttatactg 90

<210> 9
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 9
gaggtgtatg tgcccacagt gtttgagaac tatgtggcag atatcgaggt ggatggaaag 60
caggtagagt tggctttgtg ggacacagct 90

<210> 10
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 10
ggtgatgtag cctgtggaaa gacatgccta ttaatagtct tcagcaagga ccagttccca 60
gaggtgtatg tgcccacagt gtttgagaac 90

<210> 11
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 11
cccatggagc agaagctgat ctccgaggag gacctgaacc ggaagaaact ggtgattgtt 60
ggtgatgtag cctgtggaaa gacatgccta 90

<210> 12
<211> 612
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 12
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aaccgtaaac aacacgttgc tttgcttatg aattcttctg gatctactgg tttacctaaa 120

ggtgtacgaa ttacccacga aggtgcagtt acaagattct cacacgctaa ggatccaatt 180
tacggaaacc aagtttcacc tggtactgct attttaactg tcgttccgtt ccatcatgga 240
tttggaatgt ttaccacttt aggatacttt gcttgcggat accgtgttgt aatgttaaca 300
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cttgtaccaa ccttatttgc tattctcaac aagagtgaat tgatcgataa gttcgattta 420
tctaatctaa ctgaaattgc ttctggtgga gctcctttgg caaaagaagt tggcgaagca 480
gtcgctagaa gatttaatct acccggtgtc cgtcagggtt acggattaac agaaacaaca 540
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cccttattca aa 612

<210> 13
<211> 104
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 13
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aaccgtaaac aacacgttgc tttgcttatg aattcttctg gatc 104

<210> 14
<211> 104
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 14
ttggatcctt agcgtgtgag aatcttgtaa ctgcaccttc gtgggtaatt cgtacacctt 60
taggtaaacc agtagatcca gaagaattca taagcaaagc aacg 104

<210> 15
<211> 104
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 15
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ctattttaac tgtcgttccg ttccatcatg gatttggaat gttt 104

<210> 16
<211> 104
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 16

ctcaaaaaca gttcttcatc aaattttgtt aacattacaa cacggtatcc gcaagcaaag 60
tatcctaaag tggtaaacat tccaaatcca tgatggaacg gaac 104

<210> 17
<211> 104
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 17
ttgtaatgtt aacaaaattt gatgaagaac tgtttttgag aactttgcaa gattataagt 60
gtaccagtgt gattcttgta ccaaccttat ttgctattct caac 104

<210> 18
<211> 104
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 18
tttgccaaag gagctccacc agaagcaatt tcagttagat tagataaatc gaacttatcg 60
atcaattcac tcttgttgag aatagcaaat aaggttggta caag 104

<210> 19
<211> 104
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 19
aattgcttct ggtggagctc ctttggcaaa agaagttggc gaagcagtcg ctagaagatt 60
taatctaccc ggtgtccgtc agggttacgg attaacagaa acaa 104

<210> 20
<211> 104
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 20
tttgaataag ggtaccactt ttccagatgc tccaggttta tcatcacctt ctggagtaat 60
aataaatgca gatgttgttt ctgttaatcc gtaaccctga cgga 104

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 21
attaagaaac atgtagaatt 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic DNA

<400> 22
tttgaataag ggtaccactt 20